

80837
Schreiber, David

From: Ramirez, Delia
Sent: Thursday, November 21, 2002 11:59 AM
To: Schreiber, David
Subject: case 09/854844

Hi David,

I was wondering if you could do an alignment for me. It is seq id 1 against the DNA of accession XM_093852 and seq id 2 against the protein encoded in XM_093852, (LOC166414). Applicant's argue that this entry has 99% similarity to their seq id 2 but I could not find this in the first seach I did.

Thanks,

Delia

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, 10D04, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 11/21
Searcher: D. Schirber 308-492
Terminal time: 42
Elapsed time: 6
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
☒ CM-1 6A03
____ Pre-S
Type of Search
☒ N.A. Sequence
☒ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
☒ Other compus
www and

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|||||
Db 601 GAAGACAAGATTGTGCTGTGTGATCTCAAAACATGAAGGATAGTTGCAAGGGTGATTCT 660
QY 661 GGAGGGCCTCTGTCGTCTACATTGATGTGTATGGATCCAGACAGGAGTAGTAAGCTGG 720
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Db 721 GGATTAGAATGTGGTAAATCTCTTCTGGAGTCTACACCAATGTAATCTACTACCAAAAA 780
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Db 961 TGGAGATTAGTCCAGGGGCAGATRA 987

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Search completed: November 21, 2002, 14:30:56
Job time : 1 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: November 21, 2002, 14:34:26 ; Search time 0.001 Seconds
(without alignments)
113.488 Million cell updates/sec

Title: us-09-854-844-2
Perfect score: 1863
Sequence: 1 MGPAGCAFTLLLLGISVCG.....GRELTGPELLFLGDFIYNLK 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 328 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : loc166414.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749	93.9	328	1 LOC166414	ACCESSION:XP_093855

ALIGNMENTS

RESULT 1
LOC166414
LOCUS LOC166414 328 aa linear PRI 13-MAY-2002
DEFINITION similar to epidermis specific serine protease [Homo sapiens].
ACCESSION XP_093852
VERSION XP_093852.4 GI:20534016
DBSOURCE REFSEQ: accession XM_093852.4
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (residues 1 to 328)
NCBI Annotation Project.
Direct Submission
TITLE Submitted (09-MAY-2002) National Center for Biotechnology
JOURNAL Information, NIH, Bethesda, MD 20894, USA
COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was
predicted from NCBI contig NT_022851 by automated computational
analysis using gene prediction method: GenomeScan.
Also see:
Documentation of NCBI's Annotation Process

On May 13, 2002 this sequence version replaced gi:20503620.
Location/Qualifiers
1..328
/organism="Homo sapiens"

FEATURES
source

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/region_name="Trypsin"
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/db_xref="InterimID:166414"

Query Match 93.9%; Score 1749; DB 1; Length 328;
Best Local Similarity 99.4%; Pred. No. 0;
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QY 1 MGPAGCAFTLLLLGISVCGQPVYSSRVVGGODAAAGRPWQVSLHFDHNFYGGSLVSE 60
|||||
Db 1 MGPAGCAFTLLLLGISVCGQPVYSSRVVGGODAAAGRPWQVSLHFDHNFYGGSLVSE 60
|||||

QY 61 RLILTAACIQPTWTFSTVVLGSIYVSGDSSRRKRVYVSKIVHPKYQDTTADVALLKL 120
|||||
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|||||
Db 121 SSQVTFSAIPLPSVTKQLAIPPCVWTGKVKESDRDYHSALEAEVPIIDRQA 180
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|||||
Db 181 CEQLYNPICIGIFPALEPVIKEDKICAGDTQNMKDCSKGSGPLSCHIDGVWITGVVSW 240
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|||||
Db 241 GLECGKSLPGVYTNVIYOKWINATISRANNDLDFSLFPVILLSLALLCPSCAFGPNTI 300
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Db 301 HRVGTVAEAVACIQGWEENAWRFSPRGR 328
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Search completed: November 21, 2002, 14:34:27
Job time : 1 secs